In the Claims

Please cancel claims 7 and 20 without prejudice.

Please enter the following rewritten claims 1-3, 5, 6, 9, 21 and 23 as follows:

1. (Amended) A method for enriching for target DNA sequences containing at least a partial coding region for at least one specified activity in a DNA sample comprising:

a) co-encapsulating in a micro-environment selected from a liposome, gel microdrop, bead, agarose, cell, ghost red blood cell and ghost macrophage a mixture of target DNA obtained from more than one organism with a mixture of DNA probes comprising a detectable label and at least a portion of a DNA sequence encoding at least one enzyme having a specified enzyme activity;

b) incubating the co-encapsulated mixture under such conditions and for such time as to allow hybridization of complementary sequences; and

c) screening to recover the hybridized complementary sequences containing the detectable label, thereby enriching the DNA sequences containing the at least partial coding region for the specified activity in the recovered target DNA.

2. (Amended) The method of claim 1, further comprising transforming host cells with the recovered target DNA to produce an expression library of a plurality of clones.

3. (Amended) The method of claim 1, wherein the more than one organism is a plurality of microorganisms.

5. (Amended) The method of claim 2, further comprising screening the expression library for the specified enzyme activity.

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6. (Amended) The method of claim 1, wherein the screening to recover the hybridized complementary sequences comprises:

a) converting double stranded DNA into single stranded DNA;

b) recovering from the converted single stranded DNA, single stranded target DNA which hybridizes to probe DNA;

c) converting recovered single stranded target DNA to double stranded DNA; and

d) transforming a host cell with the double stranded DNA of c).

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9. (Amended) The method of claim 4, wherein the uncultured microorganisms are obtained from an environmental sample.

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21. (Amended) The method of claim 1, wherein the liposomes are prepared from one or more phospholipids, glycolipids, steroids, alkyl phosphates or fatty acid esters.

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23. (Amended) The method of claim 21, wherein the steroids are selected from the group consisting of cholesterol, cholestanol and lanosterol.

Please add the following new claims:

--27. (New) A method for enriching for target DNA sequences containing at least a partial coding region for at least one specified activity in a DNA sample comprising:

a) co-encapsulating in a micro-environment selected from a liposome, gel microdrop, cell, ghost red blood cell and ghost macrophage a mixture of target DNA obtained from more than one organism with at least one DNA probe comprising a detectable label and at least a portion of a DNA sequence encoding at least one enzyme having a specified enzyme activity;

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b) incubating the co-encapsulated mixture under such conditions and for such time as to allow hybridization of complementary sequences; and

c) screening to recover the hybridized complementary sequences containing the detectable label, thereby enriching the DNA sequences containing the at least partial coding region for the specified activity in the recovered target DNA.

28. (New) A method for enriching for target DNA sequences containing at least a partial coding region for at least one specified activity in a DNA sample comprising:

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a) co-encapsulating in a micro-environment selected from a liposome, gel microdrop, cell, ghost red blood cell and ghost macrophage a target DNA obtained from more than one organism with a mixture of DNA probes comprising a detectable label and at least a portion of a DNA sequence encoding at least one enzyme having a specified enzyme activity;

b) incubating the co-encapsulated mixture under such conditions and for such time as to allow hybridization of complementary sequences; and

c) screening to recover the hybridized complementary sequences containing the detectable label, thereby enriching the DNA sequences containing the at least partial coding region for the specified activity in the recovered target DNA.--